

*Appl. No. 09/724,910*

*Supplemental Response to Office Action dated 08/09/05*

*Supplemental Response dated February 13, 2006*

### AMENDMENTS

A complete listing and status of the claims is provided below, which replaces all previous listing of the claims. Claims 1 to 45 have been cancelled. Claims 46-51 were previously presented in Applicant's reply dated February 9, 2006.

Claims 1 – 45. (Cancelled)

46. (Previously presented) A method for processing fragment analysis data, comprising:

- receiving the fragment analysis data wherein the data represents intensity and nucleic acid fragment length information,
- presenting the fragment analysis data to a two-stage allele caller ,
  - wherein a second stage is configured to perform a second analysis that determines allele calls for the fragment analysis data and a first stage is configured to perform a first analysis to determine whether or not the fragment analysis data signal is within the second stage's operating region,
- performing said first analysis with said first stage and if said first stage determines that said fragment analysis data is within said second stage's operating region, performing said second analysis, and
- reporting the results of said first and second analysis.

47. (Previously presented) The method of claim 46 wherein said first stage is configured to determine one or more maxima of said fragment analysis data and form a first signal composed of the one or more maxima, to determine one or more minima of said first signal and to divide said first signal into one or more panels with a panel boundary located at each of the one or more minima, and then to determine if three or more panels exist.

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48. (Previously presented) The method of claim 47 wherein said second stage is configured to perform said second analysis if at least three panels exist wherein said second analysis comprises:

- determining the energy in each panel,
- defining a first panel corresponding to the panel which contains the greatest energy,
- defining a second panel corresponding to the panel which contains the second greatest energy,
- defining a third panel corresponding to the panel which contains the third greatest energy,
- performing a first test to determine if the ratio of the energy in the first panel to the energy in the second panel is above a first threshold,
- performing a second test to determine if the ratio of the energy in the third panel to the energy in the second panel is below a second threshold, and
- calling alleles in each of the first and second panels if the first and second tests are passed.

49. (Previously presented) The method of claim 48 wherein said calling alleles step comprises:

- defining a first allele in the first panel as the fragment length corresponding to the maximum intensity value in the first panel, and
- defining a second allele in the second panel as the fragment length corresponding to the maximum intensity value in the second panel.

50. (Previously presented) The method of claim 48 wherein energy is defined as the integral of the signal contained in the panel.

51. (Previously presented) A computer readable medium containing instructions for controlling a computer system to perform a method for processing fragment analysis data, the method comprising:

- receiving the fragment analysis data wherein the data represents intensity and nucleic acid fragment length information,
- presenting the fragment analysis data to a two-stage allele caller,

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- wherein a second stage is configured to perform a second analysis that determines allele calls for the fragment analysis data and a first stage is configured to perform a first analysis to determine whether or not the fragment analysis data signal is within the second stage's operating region,
- performing said first analysis with said first stage and if said first stage determines that said fragment analysis data is within said second stage's operating region, performing said second analysis, and
- reporting the results of said first and second analysis.